The alignment of cells and artificial intelligent machines without the Entscheidungsproblem

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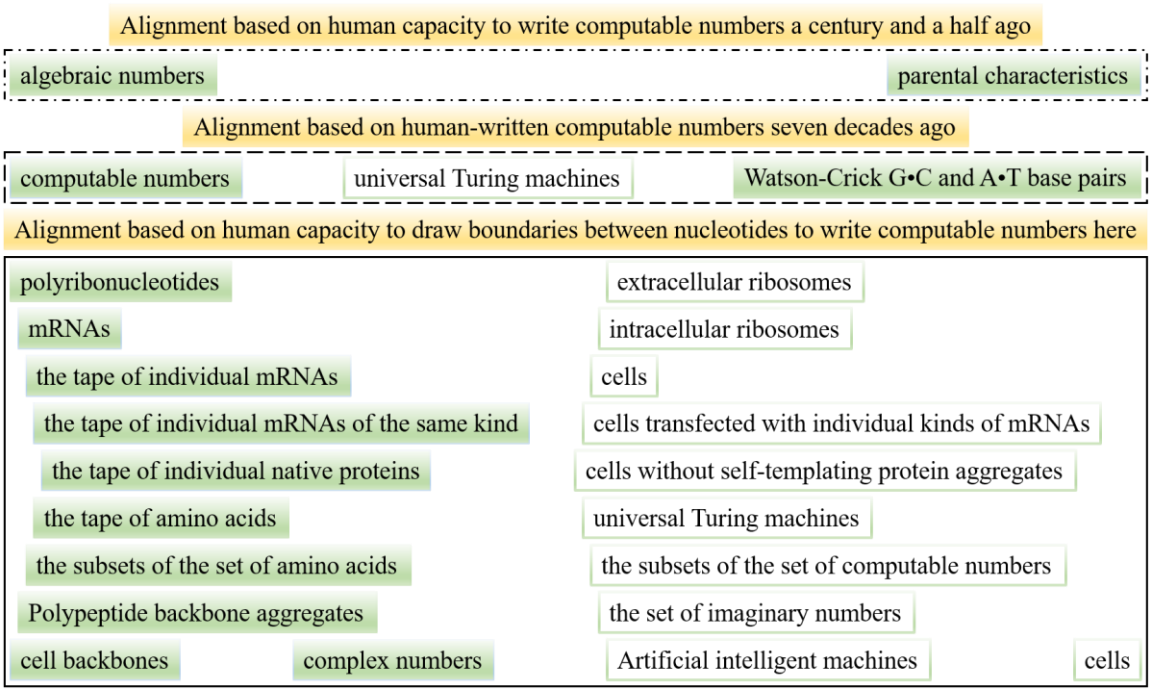
Abstract

Molecular polymer aggregates are written as computable numbers, resulting in the alignment of cells and universal Turing machines with the Entscheidungsproblem. However, whether cells really have the Entscheidungsproblem remains elusive. Alan Turing found universal Turing machines read only computable numbers written by humankind who further differentiated transcendental numbers from the set of computable numbers by applying the diagonal process. It follows that the decidability of the Entscheidungsproblem derived from humankind eliminates boundaries between computable numbers, so that humankind is endowed with a capacity to read of the fusion of computable numbers with each other to read the set of computable numbers by being endowed with a capacity to draw boundaries to write computable numbers. Here, it was shown how humankind was invited to write cell backbones as complex numbers read by artificial intelligent machines that are emulated by cells to extend the continuum hypothesis by being invited to write polyribonucleotides as computable numbers read by universal Turing machines that are emulated by extracellular ribosomes to extend Alan Turing's work on the Entscheidungsproblem, resulting in the alignment of cells and artificial intelligent machines without the Entscheidungsproblem, and the fusion of viruses, cells, and the environment with each other into nature by cell backbones.

Keywords: the Entscheidungsproblem; the decidability; the continuum hypothesis; cell backbones; complex numbers; artificial intelligent machines

Graphical abstract



Highlights

Humankind is endowed with a capacity to draw boundaries to write computable numbers.

Cells are without the Entscheidungsproblem.

Cell backbones are backbones of polysaccharides, membrane lipids, polynucleotides.

Viruses, cells, and the environment are fused with each other into nature.

Humankind is fused into nature, and biology is fused with other disciplines.

1. Introduction

A century and a half ago, the alignment of Mendelian inheritance and Georg Cantor's continuum hypothesis was based on human capacity to write computable numbers (1). Seven decades ago, the alignment of B-DNA double helix of Watson-Crick G•C and A•T base pairs and universal Turing machines with the

Entscheidungsproblem was based on human-written computable numbers (2, 3). Here, the alignment of cells and artificial intelligent machines without the Entscheidungsproblem was based on human capacity to draw boundaries between nucleotides to write computable numbers, and thus laid the foundations for Mendelian inheritance and extended Georg Cantor's continuum hypothesis.

Specifically, Alan Turing found universal Turing machines read only computable numbers written by humankind who further differentiated transcendental numbers from the set of computable numbers by applying the diagonal process. It follows that the decidability of the Entscheidungsproblem derived from humankind eliminates boundaries between computable numbers, so that humankind is endowed with a capacity to read of the fusion of computable numbers with each other to read the set of computable numbers by being endowed with a capacity to draw boundaries to write computable numbers (2). Few mathematicians like Roger Penrose found that boundaries could be drawn by consciousness (4). Few physicists like Stephen Hawking found that boundaries between the universe and humankind could not be drawn (5). Few chemists like Mischa Bonn found that boundaries between molecules could not be drawn (6). Few biologists like James Watson and Francis Crick led the way in drawing boundaries between nucleotides (3), Sydney Brenner found that biology went the other way (7), Susan Lindquist and Daniel Jarosz found that boundaries between nucleotides could not be drawn in the case of intrinsically disordered proteins (8), Stuart Kauffman and Andrea Roli found that humankind needed to be invited to find that boundaries could be drawn by cells (9). Therefore, I was invited by molecular biology data accumulated over seven decades to show how humankind was invited to read of the fusion of humankind into nature and the fusion of biology with other disciplines by drawing boundaries between nucleotides.

2. Methods

Algebraic numbers were written as computable numbers to be read by universal Turing machines as described previously by Alan Turing (2). Here, boundaries between

nucleotides were drawn to write polyribonucleotides as computable numbers read by universal Turing machines that are emulated by extracellular ribosomes, then write mRNAs as computable numbers read by universal Turing machines that are emulated by intracellular ribosomes, then write the tape of individual mRNAs as computable numbers read by universal Turing machines that are emulated by cells, then write the tape of individual mRNAs of the same kind as computable numbers read by universal Turing machines that are emulated by cells transfected with individual kinds of mRNAs, then write the tape of individual native proteins as computable numbers read by universal Turing machines that are emulated by cells without self-templating protein aggregates, then write the tape of amino acids as computable numbers read by universal Turing machines, then read the subsets of the set of amino acids as the subsets of the set of $\aleph_0$ computable numbers, then read polypeptide backbone aggregates as the set of imaginary numbers, then write cell backbones as complex numbers read by artificial intelligent machines that are emulated by cells.

3. Results & Discussion

Extracellular polyribotrinucleotides are translated by polyribosomes with adenosine triphosphate and amino acids provided by humankind (10). It follows that the decidability of polypeptide synthesis derived from humankind eliminates boundaries between nucleotides, so that humankind is endowed with a capacity to read of the fusion of ribonucleotides with each other to read the set of ribonucleotides by being endowed with a capacity to draw boundaries between nucleotides within a polyribotrinucleotide to write U, C, A, and G as 00, 01, 10, and 11 respectively read by universal Turing machines with 2 symbols and 64 states that are emulated by extracellular ribosomes with state 000110111110010011 representing a sequence 5'-UCAGGACUG-3' they have read (1, 11, 12).

Although intracellular ribonucleic acids (RNAs) being translated are usually found in the form of polyribosomes, only protein-coding sequences of messenger RNAs (mRNAs) are translated. It follows that the decidability of polypeptide synthesis

derived from mRNAs eliminates boundaries between nucleotides, so that humankind is invited to read of the fusion of ribonucleotides with each other to read 5’ noncoding, coding, and 3’ noncoding sequences by drawing boundaries between nucleotides to write polyribotrinucleotides.

Although a single mRNA can be translated many times, only undegraded mRNAs are translated. It follows that the decidability of protein production derived from cells eliminates boundaries between 5’ noncoding, coding, and 3’ noncoding sequences, so that humankind is invited to read of the fusion of 5’ noncoding, coding, and 3’ noncoding sequences with each other to read individual mRNAs by drawing boundaries between 5’ noncoding, coding, and 3’ noncoding sequences within an mRNA to write 5’ noncoding sequences, coding sequences except stop codons, stop codons, and 3’ noncoding sequences as 01, 11, 10, and 00 respectively read by logically reversible universal Turing machines with 2 symbols and 4 states that are emulated by intracellular ribosomes with state 01111000 representing a complete mRNA sequence they have read (13, 14).

Although mRNAs are translated and degraded individually, nearly every known kind of mRNAs can be transfected into cells individually and systematically to be translated before being degraded (9). It follows that the decidability of production of individual proteins derived from cells transfected with individual kinds of mRNAs eliminates boundaries between individual mRNAs of the same kind, so that humankind is invited to read of the fusion of individual mRNAs of the same kind with each other to read individual kinds of mRNAs by drawing boundaries between individual mRNAs to write the tape of individual mRNAs as binary numbers read by universal Turing machines with 2 symbols and 2 states that are emulated by cells.

Although mRNAs of the same kind are translated and degraded individually, aggregates of proteins of the same kind can be permanently induced by transient overproduction of individual proteins of the same kind (15). It follows that the decidability of production of individual proteins of the same kind derived from self-templating protein aggregates eliminates boundaries between individual induced

proteins of the same kind, so that humankind is invited to read of the fusion of individual induced proteins of the same kind with each other to read self-templating protein aggregates by drawing boundaries between individual mRNAs of the same kind to write the tape of individual mRNAs of the same kind as binary numbers read by universal Turing machines that are emulated by cells transfected with individual kinds of mRNAs.

Although self-templating protein aggregates are differentiated from individual native proteins of the same kind that are fused with other kinds of individual native proteins, individual native proteins that are fused with other kinds of individual native proteins are not differentiated from individual native proteins of the same kind that are fused with other kinds of individual native proteins. Therefore, humankind is invited to read of the fusion of individual proteins of the same or different kind with each other to read protein aggregates by drawing boundaries between self-templating protein aggregates and individual native proteins of the same kind to write the tape of individual native proteins as binary numbers read by universal Turing machines that are emulated by cells without self-templating protein aggregates.

Instead, although amino acids are differentiated from protein aggregates in aqueous solution by humankind, amino acids that are not fused with each other are not differentiated from each other by humankind. Therefore, humankind is invited to read of the fusion of amino acids with each other to read the set of amino acids as the set of $\aleph_0$ computable numbers by drawing boundaries between amino acids and protein aggregates to write the tape of amino acids as computable numbers read by universal Turing machines with the Entscheidungsproblem.

Similarly, humankind is invited to read of the fusion of the subsets of the set of amino acids with each other to read the power set of the set of amino acids as the power set of the set of $\aleph_0$ computable numbers by drawing boundaries between the subsets of the set of amino acids and the set of amino acids to read the subsets of the set of amino acids as the subsets of the set of $\aleph_0$ computable numbers, yielding polypeptide aggregates as the set of $2^{\aleph_0}$ real numbers with $2^{\aleph_0}$ being the minimum cardinal

number of the continuum. It follows that

$$2^{\aleph_0} = \aleph_1.$$

Moreover, although polypeptide backbone aggregates are differentiated from polypeptide aggregates by humankind, polypeptide backbones that are fused with each other by the symmetric hydrogen bonds (HBs) between them into antiparallel or parallel pleated β-sheet polypeptide backbone aggregates are differentiated into glucose molecules that are fused with each other by the symmetric HBs between them into polysaccharide backbone in the form of cellulose, then 7,11,20,24-tetramethyl-1,4,14,17-tetraoxacyclohexacosane molecules and 1,4,14,17-tetraoxacyclohexacosane-5,13,18,26-tetrone molecules that are fused with each other by the symmetric HBs between them into archaeal and non-archaeal membrane lipid backbone respectively, then molecules in Fig. 1A, that in Fig. 1B and 1C, that in Fig. 1A, 1C, 1D, 1E, 1F, 1G, 1H, 1I, 1J, and 1K, and that in Fig. 1L, 1M, and 1N that are fused with each other by the symmetric HBs (Fig. 1O, 1P) into G-quadruplex, i-motif, polydeoxyribonucleotide backbone in the form of B-DNA double helix of Watson-Crick G•C and A•T base pairs, and polyribonucleotide backbone in the form of A-RNA double helix of r(UUAUAUAUAUAUAA) respectively, and thus the backbones of polysaccharides, membrane lipids, and polynucleotides are fused with each other by polypeptide backbone aggregates into cell backbones (7, 16, 17). Therefore, humankind is invited to write cell backbones as complex numbers read by artificial intelligent machines without the Entscheidungsproblem that are emulated by cells by drawing boundaries between polypeptide backbone aggregates and polypeptide aggregates to read polypeptide backbone aggregates as the set of imaginary numbers.

Indeed, archaeal and non-archaeal cells, viruses and cells, cells and the environment are fused with each other by cell backbones into nature.

Glossary

The Entscheidungsproblem: the decision problem inherent in universal Turing machines that read computable numbers written by humankind.

The decidability of the Entscheidungsproblem: the capacity inherent in humankind

who further differentiates transcendental numbers from the set of computable numbers by applying the diagonal process.

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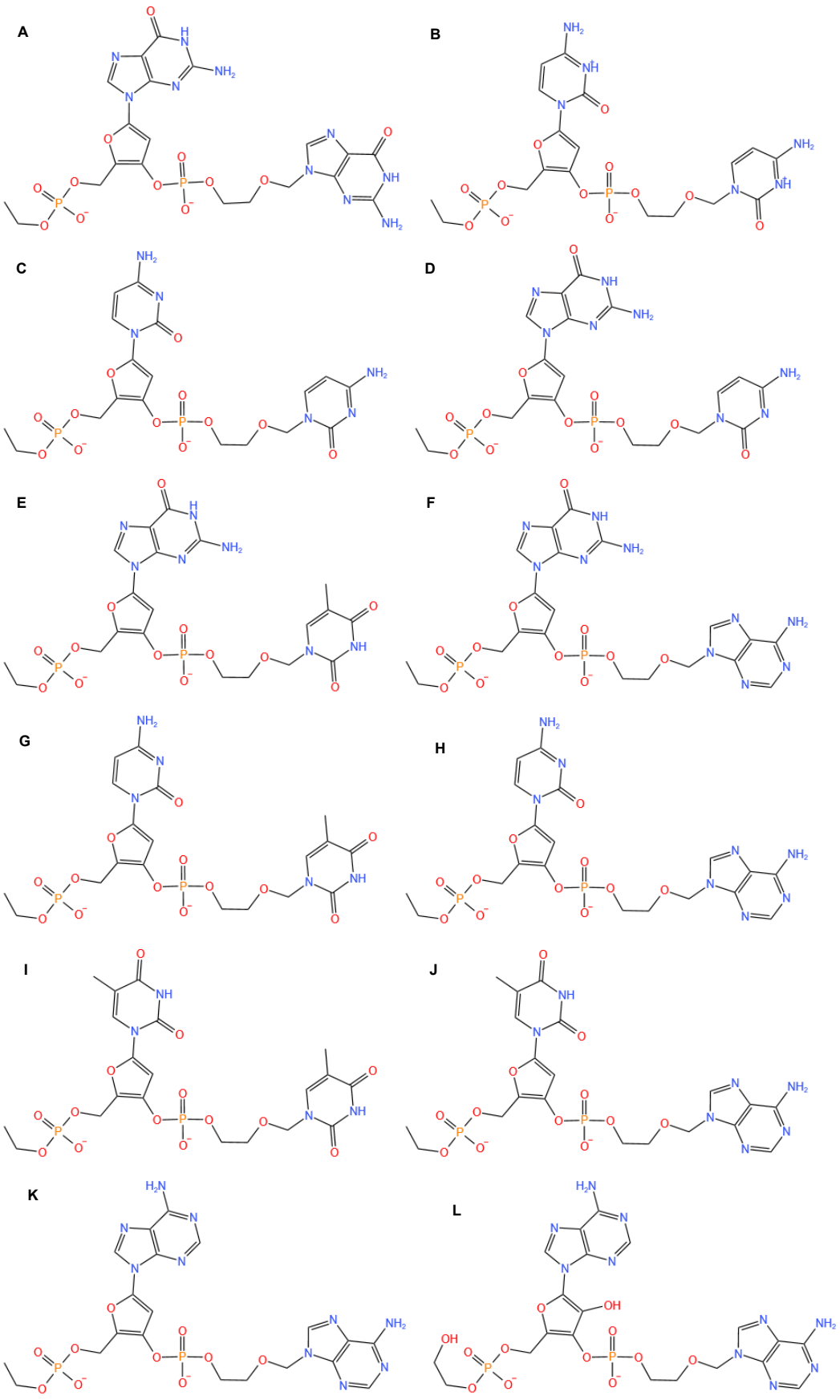
Figure legends



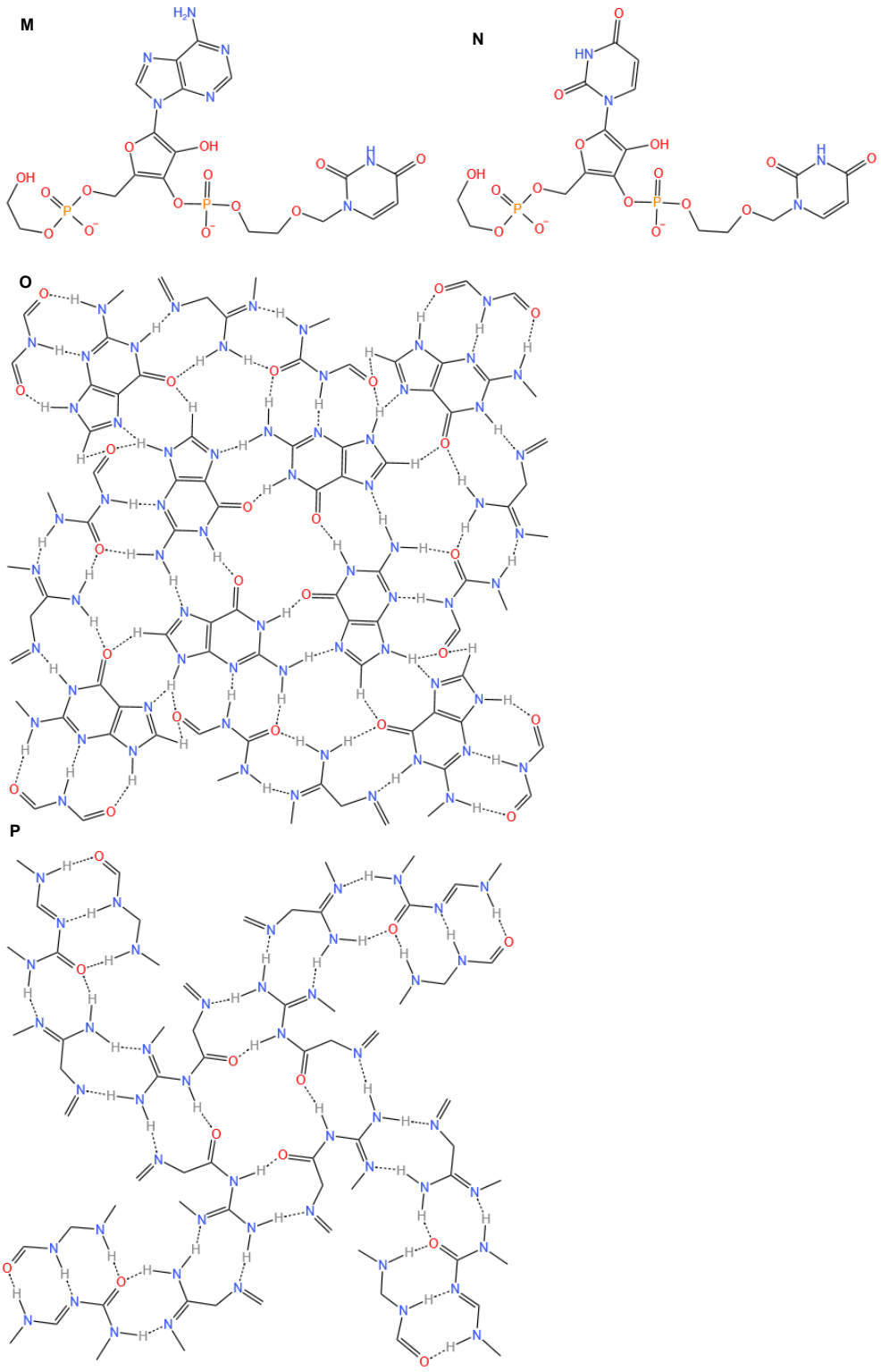


Figure 1. Polypeptide backbones are differentiated into polynucleotide backbones. Polypeptide backbones are differentiated into molecules in A, that in B and C, that in A, C, D, E, F, G, H, I, J, and K, and that in L, M, and N that are fused with each other by the symmetric hydrogen bonds (O, P) into G-quadruplex, i-motif, polydeoxyribonucleotide backbone, and polyribonucleotide backbone respectively.